

NAI Focus Group

NASA ASTROBIOLOGY INSTITUTE

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The objective of the Mixed Microbial Ecogenomics (EcoGenomics) Focus Group is to define the relationship between microbial diversity, complex gene expression patterns, and biogeochemical processes that shape planetary environments. Using the hyper-saline cyanobacterial mats of Guerrero Negro, Baja California, Mexico as a field site, this inter-team effort is characterizing biogeochemical patterns in the microbial mats with special emphasis on gradient location and shape. These measurements are being coupled with molecular-based assessments of microbial population structures and DNA microarray measurements of gene expression. The gene expression data will identify important biochemical activities that play key roles in biogeochemical gradient formation and shifts in response to transient and periodic perturbations imposed by diel cycles. The ultimate goal is to establish models that can predict the behavior of these complex systems.

Background

The questions, "Where did we come from, how did we get here, and where are we going?", embody the principle objectives of astrobiological research. Answers to the first question are rooted within the microbial world, which represented the only form of life during the initial three billion years of our evolutionary history. Ever since the origin of life, complex interactions of microorganisms with each other

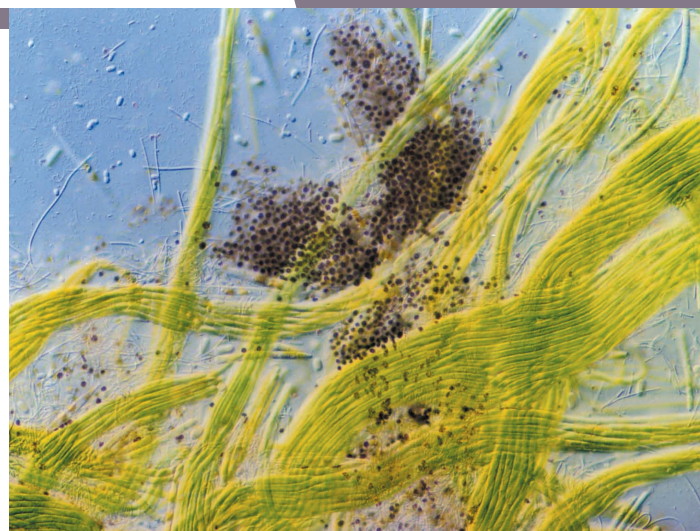
and with all other components of the biosphere have dominated the course of evolution on Earth. Even the earliest biogenic fossils (microbial mats) display integrally layered patterns of organization. This spatial structuring likely reflects functional interdependence of different microbes in early communities. Microbial creatures of untold diversity continue to dominate every corner of our biosphere, and they are likely to be the only life forms that might be encountered in other parts of our Solar System, if not the entire cosmos. Yet, there is only sparse information about the true diversity of microorganisms, including their capability to orchestrate and drive key biogeochemical cycles that shape our ever-changing planet. A more complete understanding of microbial diversity, descriptions of ecosystem-wide patterns of gene expression, and detailed analyses of biogeochemistry would provide a new foundation for interpreting paleontological and geological studies that describe Earth's early history.

The Mixed Microbial Ecogenomics Focus Group studies how microbial communities interact with the chemical and geological aspects of extreme environments such as this geothermal steam vent. Knowledge of microbial communities and their relationship to their environments can provide insight into the history of life on Earth and the potential for life elsewhere.



The NASA Astrobiology Institute (NAI) is uniquely positioned to initiate an interdisciplinary project to address these questions. With modern technology developed by the genome community, it is now possible to assess microbial diversity and the total genetic coding capacity of any particular environment. This would be based on phylogenetic surveys of ribosomal RNAs and high-throughput DNA sequencing. The EcoGenomics Focus Group has formulated a bold strategy for linking microbial gene expression patterns with particular metabolic activities that underlie central biogeochemical processes. Community DNA extracted from natural microbial populations of a selected site will be treated as a complex mixed genome. Members of the microbial community will be surveyed by analysis of rRNAs, and descriptions of potential metabolic diversity will be inferred from database analyses of several hundred thousand randomly selected DNA sequences. This large database of DNA sequences from the "mixed environmental genome" will be used to design DNA microarrays that can detect mRNA transcription patterns. With this mixed environmental genome array technology (MEGAT), tens of thousands of distinct genes of known sequence and function can be efficiently monitored. MEGAT will define changes in gene expression

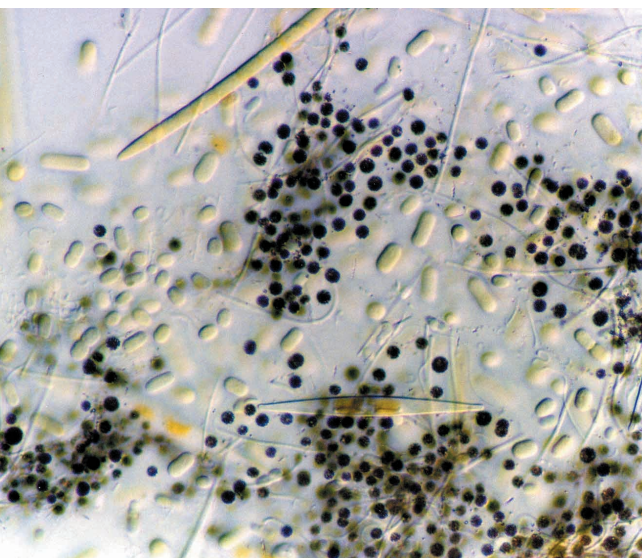
Microcoleus and purple sulfur bacteria. This microphotograph shows cyanobacteria and purple photosynthetic bacteria. This image shows a variety of microbes that are representative of a microbial ecosystem. Photo credit L. Prufert-Bebout



from a large number of environmental samples with known spatial and temporal distribution patterns in a well-structured microbial community, e.g., microbial mats or stromatolites. Results of these studies will be correlated with detailed measurements of biogeochemical gradients throughout the studied environment. The initial objective is to define biological complexity within the studied microbial system. The ultimate objective is to model how coordinated gene expression patterns observed in microbial consortia shape the environment.

Recent Activities

EcoGenomics Focus Group meetings were held in November 2000 and April 2001 to plan for a major field excursion to take place during the first two weeks of June 2001. Five primary goals were defined for this field trip: 1) establishing the microbial mat carbon and oxygen budgets, 2) characterizing populations of sulfate reducing bacteria, 3) measuring the lateral distributions of cyanobacterial populations within subtidal microbial mats, 4) conducting total microbial diversity surveys throughout the mat, and 5) characterizing the biogeochemistry of sulfur in photosynthetic microbial mats.



Photomicrograph of cyanobacteria, purple sulfur bacteria, and diatoms from microbial mats maintained in the Early Microbial Ecosystems Research Group Greenhouse Collaboratory at Ames Research Center. Photo credit: L. Prufert-Bebout